

Genstore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:42:17, Search time 18 0714 seconds
(without alignments)
58,517 Million cell updates/sec

Title: us-09-856-070-23

Perfect score: 55

Sequence: 1 ELMRLQDYEE 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 28324 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 28324

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARY

Result No.	Score	Match	Length	ID	Description
1	55	100.0	581	2 145889	ezrin - bovine
2	55	100.0	586	1 A34400	ezrin [validated]
3	55	100.0	630	2 T47177	hypothetical prote
4	52	94.5	586	1 D41129	ezrin - mouse
5	38	69.1	130	2 H84133	hypothetical prote
6	38	69.1	150	2 C97449	hypothetical trans
7	38	69.1	150	2 AF2677	transcription fact
8	37	67.3	111	2 H28577	hypothetical prote
9	37	67.3	321	2 H82832	protein export mem
10	37	67.3	337	1 A70364	conserved hypotet
11	37	67.3	1058	2 S65460	apolipoprotein B -
12	36	65.5	253	2 H83244	conserved hypotet
13	36	65.5	284	2 H84700	probable adenylyt
14	36	65.5	304	2 C92554	conserved hypotet
15	36	65.5	451	2 S01092	conserved hypotet
16	36	65.5	2472	2 A35715	iodin alpha chain
17	36	65.5	2477	1 S7CBA	iodin alpha chain
18	35	63.6	66	2 H84093	spectrin alpha cha
19	35	63.6	152	2 T36984	hypothetical prote
20	35	63.6	221	2 H97212	hypothetical prote
21	35	63.6	477	2 T01828	probable phosphor
22	35	63.6	892	1 P4U7AA	hypothetical prote
23	35	63.6	964	2 P59404	alpha actinin 1
24	35	63.6	4574	2 G02520	plectin isoform p1
25	35	63.6	4684	2 A59404	plectin - human
26	35	63.6	4687	1 A39638	plectin - rat
27	34	61.8	105	1 H69333	conserved hypotet
28	34	61.8	250	2 H84212	hypothetical prote
29	34	61.8	327	2 T47000	ethanolamine phosph

ALIGNMENTS

RESULT 1

145889

ezrin - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 14-Aug-1999

C:Accession: 145889

R:Rergson, C.M.; Zhao, H.; Saitoh, K.; Duman, R.S.; Nustler, E.J.

Mol. Cell. Neurosci. 4, 64-73, 1993

A:Title: Ezrin and osteonectin, two proteins associated with cell shape and growth, a

A:Reference number: 145889

A:Accession: 145889

A:Status: preliminary; translated from GK/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-581 <HCK>

A:Cross-references: GB:M08498; NID:q289407; FID:AAA40510.1; FID:q289408

C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

F:7-291/domain: protein 4.1 membrane-binding domain homology <841>

Query Match 100.0%, Score 55, HA 2, Length 581;

Best local Similarity 100.0%; Pred. No. 0.017;

Matches 11, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QV 1 ELMRLQDYEE 11

DB 346 ELMRLQDYEE 356

RESULT 2

A34400

ezrin [validated] - human

R:Alternate names: cytovillin, p81 protein, villin 2

C:Species: Homo sapiens (man)

C>Date: 22 Jan 1990 #sequence_revision 14 Jul 1994 #text_change 08 Dec 1990

C:Accession: A34400; S04263; E61002

R:Turkmen, S.; Winkler, R.; Fakkauer, R.; Grieselink, K.H.; Wahlstrom, T.; Vaheeri, A.

J Biol Chem 269, 16727-16732, 1994

A:Title: Cytovillin, a microvillin-like protein, is a 75,000 protein, cDNA sequence, prokaryotic exp

A:Reference number: A34400; M010-85380259; FID:2674140

A:Accession: A34400

A:Molecule type: mRNA

A:Residues: 1-586 <TUR>

A:Cross-references: CH:05921

A:Note: the translation of residues 1-11 is not given

A:Note: parts of this sequence were confirmed by protein sequencing

R:Gould, K.L.; Bretschneider, A.; Esch, F.S.; Hunter, T.

EMBO J. 8, 4133-4142, 1989

A:Title: cDNA cloning and sequencing of the protein tyrosine kinase substrate, ezrin,

A:Reference number: S09263; M010-90076135; FID:2591371

A:Accession: S09263

A:Molecule type: mRNA

A:Residues: 2-580 <GOUL>

A:Cross-references: GB:A51531; NID:q31282; FID:AAA35893.1; FID:q31283

Kilbaw, G.; Rasmussen, H.H.; Van den Hulst, M.; Van Damme, J.; Puyfer, M.; Gesser, B.; G
Electrophoresis 11, 528-536, 1990
A:Title: Two-dimensional gel electrophoresis, protein electrophoretic and microsequencing
A:Reference number: A61002; PMID:91031404; PMID:169755
A:Accession: E61002
A:Molecule type: protein
A:Residues: 255-263; 194, 196, 199, 201, 254, 270 <BA>
A:Note: It is not certain whether this material represents ezrin or radixin (see entry A
A:Comment: This material corresponds to transfected epithelial amino cell (AMA) database
C:Keywords: actin binding; cytoskeleton; experimental; MAT
F:7-291/Domain: protein 4.1 membrane binding domain, homology <H1>
F:553-586/Region: actin binding #status predicted
F:66/Binding site: phosphate (Ser) (covalent) #status predicted
F:214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted
A:Gene: GH:VIL2
A:Cross-references: GH:120489; GIM:123900
A:Map position: 6q25-6q26
C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
C:Keywords: actin binding; cytoskeleton; membrane-associated protein; phosphoprotein
F:2-586/Product: ezrin; cytoskeleton; cytosol; membrane-associated protein; phosph
F:7-291/Domain: protein 4.1 membrane binding domain, homology <H1>
F:553-586/Region: actin binding #status predicted
F:66/Binding site: phosphate (Ser) (covalent) #status predicted
F:214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted
Query Match 100.0%; Score 55; DB 1; Length 586;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELMRLQDYEE 11
Db 1111111111
1b 446 ELMRLQDYEE 456
RESULT 3
T47177
hypothetical protein DKFZp762H157.1 human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Apr-2000 #sequence_revision 20 Apr 2000 #text_change 92-Sep 2000
C:Accession: T47177
Submitted to the Protein Sequence Database, March 2000
A:Reference number: 224377
A:Accession: T47177
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-640 <AA>
A:Cross-references: EMBL:AL162086
A:Experimental source: adult melanoma (MeWo cell line); clone DKFZp762H157
C:Genetics:
C:Superfamily: ezrin; protein 4.1 membrane binding domain homology
Query Match 100.0%; Score 55; DB 2; Length 640
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELMRLQDYEE 11
Db 390 ELMRLQDYEE 400
RESULT 4
H41129
ezrin - mouse
N:Alternate names: cytovillin; p41 protein; radixin; villin 2
C:Date: 04-Aug-1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
C:Accession: H41129; EMBL:U01001; EMBL:U01001; S24200
C:Pinayama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.;
J. Cell Biol. 115, 1039-1048, 1991
A:Title: Radixin is a novel member of the band 4.1 family.
A:Reference number: A41129; PMID:92064635; PMID:1955455
A:Accession: H41129
A:Molecule type: mRNA
A:Residues: 1-586 <AA>

A:Cross-references: EMBL:X60671; NID:q50880; PIDD:CAA43086.1; PIDD:q50881
R:Ecrtion, M.; Burgess, W.H.; Chen, D.; Druker, B.J.; Bretscher, A.; Samelson, L.E.
J. Immunol. 149, 1847-1852, 1992
A:Title: Identification of ezrin as an 81-kDa tyrosine-phosphorylated protein in T cell
A:Reference number: A46501; PMID:92388649; PMID:1381389
A:Accession: C46501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 412-426 <EE>
A:Experimental source: MRL lpr/lpr, T-cells
A:Note: sequence extracted from NCBI backbone (NCBI:112948)
A:Accession: A46501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-33; 150, 152, 155 <EE>
A:Experimental source: MRL lpr/lpr, T-cells
A:Note: sequence extracted from NCBI backbone (NCBI:112948)
A:Accession: H46501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 59-57, 148, 150, 152, 155 <EE>
A:Experimental source: MRL lpr/lpr, T-cells
A:Note: sequence extracted from NCBI backbone (NCBI:112940)
C:Comment: This protein is located in microvilli and is proposed to play a role in mo
C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
C:Keywords: actin binding; cytoskeleton; cytosol; membrane-associated protein; phosph
F:7-291/Domain: protein 4.1 membrane-binding domain homology <H1>
F:553-586/Region: actin binding #status predicted
F:66/Binding site: phosphate (Ser) (covalent) #status predicted
F:214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted
Query Match 94.5%; Score 52; DB 1; Length 586;
Best Local Similarity 90.9%; Pred. No. 0.065;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELMRLQDYEE 11
Db 346 ELMRLQDYEE 356
RESULT 5
H84133
hypothetical protein BH3872 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84133
K:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A84655; PMID:10512562; PMID:1058132
A:Accession: H84133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-130 <STO>
A:Cross-references: GH:AP001520; GH:BA0000004; NID:g10176401; PIDD:HAH0759.1; GSPPH:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3872
Query Match 69.1%; Score 38; DB 2; Length 140;
Best Local Similarity 87.5%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 LRLQDYEE 11
Db 78 LRLQDYEE 85
RESULT 6
C97449
hypothetical transcription regulator y4td [imported] - Agrobacterium tumefaciens (str
C:Species: Agrobacterium tumefaciens

A:Residues: 1-111 <LA2>
A:Cross-references: EMBL:AF020713; NID:g3025478; PID:g3025571; PDB:AACI3066, 1
F:Kunst, F., Gaspawara, N., Masaki, T., Albertini, A.M., Allouhi, C., Arevedo, V., Her
C:Brink, S.; Krell, D.H.; S. Masaki, T.V. Chanderlin, R. Capasano, V. Carter, N.M.;
A:Ethlich, S.B.; Hammarich, B.L.; Entian, K.B.; Hittinger, J.; Hubert, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Feiler, G.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gal
lechi, J.; Harwood, C.R.; Heuvel, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Iiallo, M.
Koetzel, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidos, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y.; Miyagawa, A.; Odawara, A.; Ouedda, H.; Park, S.H.; Parro, V.; Kohl, T.M.; Portote
Pier, M.; Pivetta, F.; Pochet, F.; Roeder, R.; Rose, M.; Sadashige, Y.; Satoh, T.; Scari
A:Authors: Schiele, S.; Schroeter, R.; Seutonne, F.; Sekiguchi, J.; Sekowska, A.; Se
kenichi, M.; Tamayoshi, A.; Tanaka, T.; Terstira, P.; Tognoni, A.; Tegada, K.; Yoshi
I.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Title: The complete genome sequence of the Gram positive bacterium Bacillus subtilis
A:Reference number: A66680; MIPS:G0404043; PMID:9494477
A:Accession: E69918
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-111 <UN>
A:Cross-references: GR:Z99114; GR:Z99115; GR:A000126; NID:G2634478; PDB:CAR1492, 1;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yopW
C:Superfamily: Bacillus subtilis phage SPB2 hypothetical protein yopW

Query Match: 67.3%, Score 37, DB 2, Length 111;
Best Local Similarity: 63.6%; Pred. No. 7.5;
Matches: 7, Conservative: 1, Mismatches: 3, Gaps: 0;

Oy 1 ELMRLQDYEE 11
II : III
Db 20 ELKLETSDFE 30

RESULT 9
H82932
Protein expert: membrane protein: XF0226 [imported] Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Accession: B82832
C:Date: 18-Aug-2000 #sequence_revision:20-Aug-2000 #text_change:02-Sep-2000
R:anonymized, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A83515; MIPS:20465717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: B82832
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-321 <SIM>
A:Cross-references: GR:AF003876; GB:A6003849; NID:g9105031; PDB:AAF84039, 1; GSPDR-GN
R:Simpson, A.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Apencio, M.; Alvares, P.; B
Briões, M.F.S.; Buco, M.P.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
A:Authors: Ferreira, C.; Dutra, R.; Facinelli, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, E.C.; Miyaki, C.
Rodrigues, V.; Rosa, A.I.; de M. do Rosário, V.F.; de Sa, P.G.; Santelli, R.C.; Palmeri,
A:Authors: da Silva, A.P.; da Silva, F.F.; da Silva, A.W.; Silva Jr., W.A.; da Silv
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0226
C:Superfamily: Escherichia coli preprotein translocase chain sect

Query Match: 67.3%, Score 37, DB 2, Length 321;

Best Local Similarity 63.6%; Score 47; DR 1; Length 337;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELMLRLQDYEE 11
DB 91 ELMLRLQDYAE 101
|||||
|

RESULT 10
A70464
conserved hypothetical protein aq_729 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: A70464
C:Bankert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi
V.
Nature 392, 454-458, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70464; MIM:6816666; PMID:9537420
A:Accession: A70464
A:Status: preliminary; nucleic acid sequence not shown, translation not shown
A:Molecule type: DNA
A:Residues: 1-337 <ACF>
A:Cross-references: GB:AF000705; GB:AE000557; NID:q2983310; PIDN:AA066914.1; PID:q298332
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_729
C:Superfamily: conserved hypothetical protein MJ0674

Query Match 67.3%; Score 47; DR 1; Length 337;
Best Local Similarity 77.8%; Score 25; DR 2; Length 337;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMLRLQDY 9
DB 150 EVMLELQDY 158
|||||
|

RESULT 11
S65460
apolipoprotein B - Atlantic salmon (fragment)
C:Species: Salmo salar (Atlantic salmon)
C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 13-Aug-1999
C:Accession: S65460; I51362
C:Bank, P.J.; Derjovskaya, E.; Cannon, P.
Eur. J. Biochem. 230, 45-51, 1995
A:Title: Presence of an extended duplication in the putative low-density-lipoprotein re
A:Reference number: I51362; MIM:5542454; PMID:7541349
A:Accession: S65460
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1058 <HAB>
A:Cross-references: EMBL:881856; NID:q854519; PIDN:CAAS7444.1; PID:q8545420
A:Experimental source: liver
C:Genetics:
A:Gene: apob
C:Superfamily: apolipoprotein B
C:Keywords: calcium; cholesterol metabolism; glycoprotein; intestine; LDL;

Query Match 67.3%; Score 47; DR 2; Length 1058;
Best Local Similarity 63.6%; Score 87; DR 7; Length 1058;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELMLRLQDYEE 11
DB 1014 ETOLKLHYYEE 1024
|||||
|

RESULT 12
A83244
conserved hypothetical protein PA3198 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: A83244
R:Stover, C.K.; Plam, X.G.; Erwin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.L.;
adman, S.; Yuan, Y.; Brody, L.L.; Cowley, S.N.; Folger, K.K.; Kas, A.; Jarboe, K.; L
; Lory, S.; Olson, M.V.
Nature 406, 954-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MIM:20437337; PMID:10984043
A:Accession: A83244
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <SIO>
A:Cross-references: GB:AE004744; GB:AE004091; NID:q949417; PIDN:AA06486.1; GSPUR:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3198

Query Match 65.5%; Score 46; DR 2; Length 250;
Best Local Similarity 70.0%; Score 28; DR 2; Length 250;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMLRLQDYEE 10
DB 88 ELMLRLQDYEE 97
|||||
|

RESULT 13
D84790
probable adenylate kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 03-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84790
C:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayama, T.; Tallon,
cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ventor
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MIM:20083487; PMID:10617147
A:Accession: D84790
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-284 <STP>
A:Cross-references: GB:AF000204; NID:q4006480; PIDN:AA098046.1; GSPUR:GN00139
C:Genetics:
A:Gene: At2g37250
A:Map position: 2

Query Match 65.5%; Score 36; DR 2; Length 284;
Best Local Similarity 87.5%; Score 32; DR 3; Length 284;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ELRLQDYEE 11
DB 271 ELRLQDYEE 278
|||||
|

RESULT 14
G82554
conserved hypothetical protein X82451 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: G82554
C:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MIM:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59428 below
A:Accession: G82554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <SIM>
A:Cross-references: GB:AF004054; GB:AE003849; NID:q9107645; PIDN:AA085250.1; GSPUR:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Accencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 Submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Fairo, J.A.; Flaga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kompor, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, R.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miranda, E.C.; Miyaki, C.Y.
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, P.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.F.; de Sa, P.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Ishihako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski Almeida, S.; Vettore, A.L.;
 A:Reference number: A59428
 A:Contents: annotation
 C:Genetics:
 C:Gene: XP2451

Query Match 65.5% Score 36; DB 2; Length 338;
 Best Local Similarity 70.0%; Pred. No. 39;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELMRLQDYE 10
 ||| |||:
 DB 171 ELVRLQDYE 180

RESULT 15

S01092

fodrin alpha chain (clone alpha-2) - African clawed frog (fragment)

N:Alternate names: nonerythroid spectrin alpha chain

C:Species: Xenopus laevis (African clawed frog)

C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 20-Jun-2000

C:Accession: S01092

R:Gibbelhaus, D.H.; Velus, H.D.; Henchman, S.K.; Moon, R.T.

J. Cell Biol. 105, 843-853, 1987

A:Title: Changes in the expression of alpha-fodrin during embryonic development of xenop

A:Reference number: S01091; MIMD-87368385; PMID-3040772

A:Accession: S01092

A:Molecule type: mRNA

A:Residues: 1-454 <GIF>

A:Cross-references: EMBL:X06042; NID:964700; PIDN:CAA29435.1; PID:q1334648

C:Superfamily: spectrin alpha chain, calmodulin repeat homology; SH3 homology; spectrin/

C:Keywords: actin binding; EF hand

F:5 109/Domain: spectrin/dystrophin repeat homology <SP6>

F:110-225/Domain: spectrin/4.1.1:phi repeat homology <SF7>

F:216-321/Domain: spectrin/jysticphi repeat homology <SP8>

F:407-454/Domain: SH3 homology <SH3>

Query Match 65.5% Score 36; DB 2; Length 454;

Best Local Similarity 63.6%; Pred. No. 54;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELMRLQDYE 11
 ||| |||:
 DB 403 ELVRLQDYE 413

Search completed: January 16, 2003, 16:57:52

Job time : 19.0714 secs

